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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:21:33 ; Search time 11 seconds
(without alignments)
20.462 Million cell updates/sec

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Perfect score: 69
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Scoring table: BLOSUM62
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Searched: 109717 seqs, 17314136 residues

Total number of hits satisfying chosen parameters: 109717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	36	52.2	255	9	US-09-989-293A-287
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24	36	52.2	455	9	US-09-898-234-2	Sequence 17, Appl
25	36	52.2	455	9	US-09-898-234-17	Sequence 5, Appl
26	36	52.2	455	9	US-09-756-854-5	Sequence 27, Appl
27	36	52.2	455	9	US-09-899-429A-2	Sequence 5, Appl
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42	36	52.2	455	12	US-10-120-397-2	Sequence 2, Appl
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44	36	52.2	469	9	US-09-989-293A-289	Sequence 289, App
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ALIGNMENTS

RESULT 1
US-09-864-761-48620
Sequence 48620, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hank, David R.
APPLICANT: Hank, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
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Db 21 YEKMKRKILEN 31
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US-09-822-263-14
; Sequence 14, Application US/09822263
; Patent No. US20020036598A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Verneil, Corine
; APPLICANT: Shimkets, Richard A
; APPLICANT: Burgess, Catherine
; APPLICANT: Spletke, Kimberly
; APPLICANT: Tchiernev, Velizar T
; TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and polypeptides Encoded Th
; FILE REFERENCE: 15966-572 CIP1
; CURRENT APPLICATION NUMBER: US/09/822,263
; PRIOR FILING DATE: 2001-06-15
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; Sequence 287, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 2001-11-14
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 Best Local Similarity 71.4% Pred. No. 1e+02;
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 Db 42 YKKMENE 48

RESULT 4
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 ; Sequence 287; Application US/09989293A
 ; Patent No. US20020177164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Keyln P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match

Best Local Similarity 52.2%; Score 36; DB 9; Length 255;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKMKK 9
|||||:
Db 42 YKKMENE 48

RESULT 5

US-09-989-735-287
; Sequence 287, Application US/09989735
; Publication No. US20020193295A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Bolstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter

;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tamas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C61
;; CURRENT APPLICATION NUMBER: US/09/989,735
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 9; Length 255;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKWKNK 9
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 Db 42 YKKWENE 48

RESULT 6
 US-09-990-444-287
 ; Sequence 287, Application US/09990444
 ; Publication No. US20020193300A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Bolstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Geriltsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J Christopher
 ; APPLICANT: Gunney, Austin L.
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 ; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 9; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 YKKWKNK 9
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Db 42 YKKWENE 48

RESULT 7
US-09-989-722-287
Sequence 287, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P163
CURRENT APPLICATION NUMBER: US/09/989,722
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
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PRIOR APPLICATION NUMBER: 60/090349
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PRIOR APPLICATION NUMBER: 60/090435
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690

PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YKKWKNK 9
Db 42 YKKWENE 48

RESULT 8
US-09-989-723-287
Sequence 287, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Asikenzai, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
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PRIOR APPLICATION NUMBER: 60/091978
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Caps 0;

OY 3 YKKWKNK 9
|||||:
Db 42 YKKWKNK 48

RESULT 9
US-09-989-279-287
Sequence 287, Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2% Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 YKKMKK 9
Db 42 YKKWNE 48

RESULT 10
US-09-989-727-287
Sequence 287, Application US/0989727
Patent No. US20020072497A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC65
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,727
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/091633
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKWKMK 9
||||:|
Db 42 YKKWENE 48

RESULT 11
US-09-989-731-287
Sequence 287, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C70
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-09
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;; PRIOR APPLICATION NUMBER: 60/091982
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;; PRIOR APPLICATION NUMBER: 60/092182

;; PRIOR FILING DATE: 1998-07-09
Query Match 52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e-02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 3 YKKMKK 9
||||:|
Db 42 YKKMNE 48
RESULT 12
US-09-989-732-287
; Sequence 287; Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0;

DB 42 YKKWENE 48

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RESULT 13
US-09-991-073-287
Sequence 287, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC15
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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Query Match 52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 42 YKKWENE 48

RESULT 14
US-09-990-442-287
; Sequence 287, Application US/09990442

PRIOR APPLICATION NUMBER: 60/090254
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730PIC8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKKKNK 9
Db 42 YKKWNE 48

RESULT 15

US-09-991-163-287

Sequence 287, Application US/09991163

Patent No. US20020132253A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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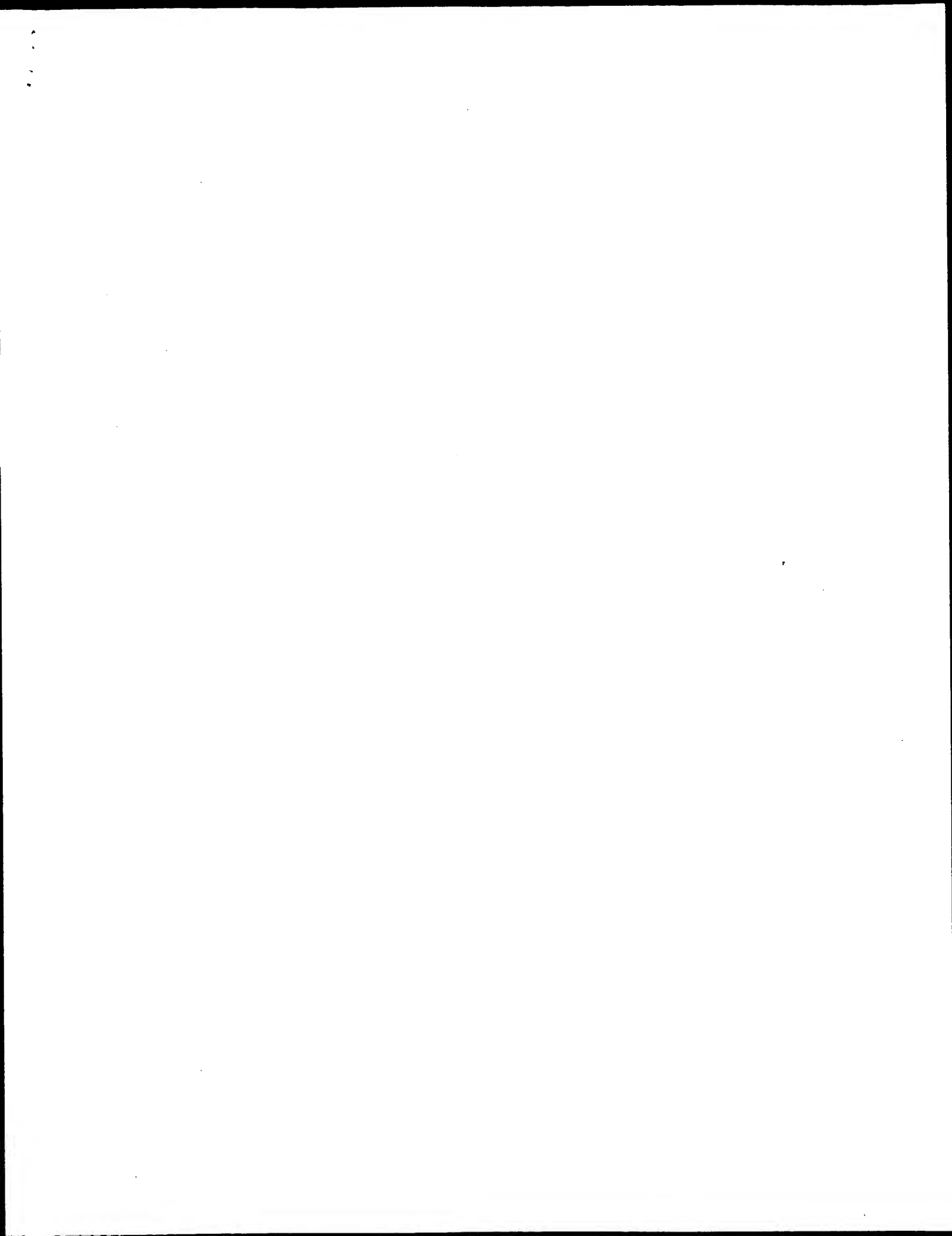
Query Match 52.2%; Score 36; DB 10; Length 255;

Best Local Similarity 71.4%; Pred. No. 1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKKNNK 9
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 Db 42 YKKKNNK 48

Search completed: December 30, 2002, 16:23:42
 Job time : 12 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:18:08 : Search time 35 Seconds

(without alignments)
49,493 Million cell updates/sec

Title: US-09-648-816b-9

Perfect score: 1 ALYKKMKNLKLS 13

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	13	20	AAV57471
2	56	81.2	18	20	AAV57472
3	55	79.7	14	20	AAV57470
4	53	76.8	18	20	AAV57465
5	53	76.8	19	20	AAV57499
6	53	76.8	19	20	AAV57501
7	53	76.8	20	20	AAV57502
8	53	76.8	25	20	AAV57496
9	53	76.8	35	20	AAV57497
10	49	71.0	18	20	AAV57500

11	49	71.0	18	20	AAV57504	Antimicrobial pept
12	48	69.6	13	20	AAV57468	Antimicrobial pept
13	46	69.6	14	20	AAV57467	Antimicrobial pept
14	47	68.1	13	20	AAV57466	Antimicrobial pept
15	47	68.1	18	20	AAV57503	Antimicrobial pept
16	44	63.8	798	21	AAV57501	Arabidopsis thalia
17	44	63.8	925	21	AAV57502	Arabidopsis thalia
18	44	63.8	1002	21	AAV57500	Arabidopsis thalia
19	43	62.3	18	12	AAV57497	Arabidopsis thalia
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21	43	62.3	18	12	AAV57495	Arabidopsis thalia
22	43	62.3	18	12	AAV57494	Arabidopsis thalia
23	43	62.3	18	12	AAV57493	Arabidopsis thalia
24	43	62.3	19	21	AAV57492	Arabidopsis thalia
25	42	60.9	13	20	AAV57469	Antimicrobial pept
26	42	60.9	60	22	AAV57468	Antimicrobial pept
27	42	60.9	132	23	AAV57467	Antimicrobial pept
28	42	60.9	1971	21	AAV57466	Antimicrobial pept
29	42	60.9	1971	22	AAV57465	Antimicrobial pept
30	42	60.9	1971	22	AAV57464	Antimicrobial pept
31	41	59.4	213	23	AAV57463	Antimicrobial pept
32	41	59.4	314	18	AAV57462	Antimicrobial pept
33	41	59.4	314	23	AAV57461	Antimicrobial pept
34	41	59.4	356	23	AAV57460	Antimicrobial pept
35	41	59.4	398	18	AAV57459	Antimicrobial pept
36	41	59.4	415	22	AAV57458	Antimicrobial pept
37	41	59.4	415	22	AAV57457	Antimicrobial pept
38	40	58.0	18	20	AAV57456	Antimicrobial pept
39	40	58.0	127	20	AAV57455	Antimicrobial pept
40	39	56.5	18	12	AAV57454	Antimicrobial pept
41	39	56.5	18	12	AAV57453	Antimicrobial pept
42	39	56.5	18	12	AAV57452	Antimicrobial pept
43	39	56.5	20	12	AAV57451	Antimicrobial pept
44	39	56.5	23	12	AAV57450	Antimicrobial pept
45	39	56.5	115	18	AAV57449	Antimicrobial pept

ALIGNMENTS

RESULT 1
AAV57471
ID AAV57471 standard; Peptide: 13 AA.
AC AAV57471;
XX
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-7 SEQ ID NO:9.
XX
XX Antimicrobial: metapetide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
XX W09942119-A1.
XX
XX
PD 26-AUG-1999.
XX
XX
PF 17-FEB-1999; 99W0-US03350.
XX
XX
PR 18-FEB-1998; 98US-0025319.
XX
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Shen AJ;
XX
XX WPI: 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
XX
XX against bacteria and fungi

PS Disclosure: Page 110; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBBZBXXB, BXZXB, BXZXXB, XBBXXBBX and BXXZBXXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXB, XBBXXBBX, BXBXBX, XBBXXBB, and
 CC XBBXXBBXXZBXX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.

SO Sequence 13 AA;

Query Match 100.0%; Score 69; DB 20; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALYKKMKNLKLS 13
 |||||
 DB 1 ALYKKMKNLKLS 13

RESULT 2
 AAY57472
 ID AAY57472 standard; Peptide: 18 AA.

XX AAY57472:
 AC 25-FEB-2000 (first entry)
 DT 25-FEB-2000 (first entry)
 XX Antimicrobial peptide RP-8 SEQ ID NO:10.
 DE Antimicrobial peptide RP-8 SEQ ID NO:10.
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX Synthetic.
 OS Oryctolagus cuniculus.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 PN 26-AUG-1999.
 PD 26-AUG-1999.
 XX 17-FEB-1999; 99WO-US03350.
 PF 17-FEB-1999; 99WO-US03350.
 PR 18-FEB-1998; 98US-0025319.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Shen AJ;
 PI WPI: 1999-527417/44.
 DR WPI: 1999-527417/44.
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi -
 PS Disclosure: Page 111; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBBZBXXB, BXZXB, BXZXXB, XBBXXBBX and BXXZBXXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXB, XBBXXBBX, BXBXBX, XBBXXBB, and

CC XBBZBXXBXXZBXX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.

SO Sequence 18 AA;

Query Match 81.2%; Score 56; DB 20; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.068;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYKKMKNLKRS 13
 |||||
 DB 2 LYKKMKNLKRS 13

RESULT 3
 AAY57470
 ID AAY57470 standard; Peptide: 14 AA.

XX AAY57470:
 AC 25-FEB-2000 (first entry)
 DT 25-FEB-2000 (first entry)
 XX Antimicrobial peptide RP-6 SEQ ID NO:8.
 DE Antimicrobial peptide RP-6 SEQ ID NO:8.
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX Synthetic.
 OS Oryctolagus cuniculus.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 PN 26-AUG-1999.
 PD 26-AUG-1999.
 XX 17-FEB-1999; 99WO-US03350.
 PF 17-FEB-1999; 99WO-US03350.
 PR 18-FEB-1998; 98US-0025319.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Shen AJ;
 PI WPI: 1999-527417/44.
 DR WPI: 1999-527417/44.
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi -
 PS Disclosure: Page 109; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBBZBXXB, BXZXB, BXZXXB, XBBXXBBX and BXXZBXXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXB, XBBXXBBX, BXBXBX, XBBXXBB, and
 CC XBBZBXXBXXZBXX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.

SO Sequence 14 AA;

Query Match 79.7%; Score 55; DB 20; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYKKMKKLLK 12
| | | | | | | |
DB 2 LYKKMKKLLK 12

RESULT 4

AAV57465
ID AAV57465 standard; Peptide; 18 AA.

AC AAV57465;

DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-1 SEQ ID NO:3.

KW Antimicrobial; metapeptide; PMF-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

OS Synthetic.

OS Oryctolagus cuniculus.

PN WO942119-A1.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03350.

PR 18-FEB-1998; 98US-0025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

DR WPI: 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active
against bacteria and fungi -

PS Claim 17; Page 106; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXB, BXZXZXB, XBBZXBXB and BBXZBBXZ; and (b) a second peptide template XBBXB and their derivatives selected from XBBZXBBXBXBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent sequences used in the exemplification of the present invention.

SQ Sequence 18 AA:

Query Match 76.8%; Score 53; DB 20; Length 18;

Best Local Similarity 84.6%; Pred. No. 0.19;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKMKKLLKS 13
| | | | | | | |
DB 1 ALYKKMKKLLKS 13

RESULT 5
AAV57499
ID AAV57499 standard; Peptide; 19 AA.

AC AAV57499;

DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide 0C-RP-1 SEQ ID NO:37.

KW Antimicrobial; metapeptide; PMF-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

OS Synthetic.

OS Oryctolagus cuniculus.

PN WO942119-A1.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03350.

PR 18-FEB-1998; 98US-0025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

DR WPI: 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active
against bacteria and fungi -

PS Disclosure: Page 58; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXB, BXZXZXB, XBBZXBXB and BBXZBBXZ; and (b) a second peptide template XBBXB and their derivatives selected from XBBZXBBXBXBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent sequences used in the exemplification of the present invention.

SQ Sequence 19 AA:

Query Match 76.8%; Score 53; DB 20; Length 19;

Best Local Similarity 84.6%; Pred. No. 0.2;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKMKKLLKS 13
| | | | | | | |
DB 2 ALYKKMKKLLKS 14

RESULT 6

AAV57501
ID AAV57501 standard; Peptide; 19 AA.

AC AAV57501;

DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.

KM Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 OS Synthetic.
 XX Oryctolagus cuniculus.
 PN WO9942119-A1.
 PD 26-AUG-1999.
 PF 17-FEB-1999; 99WO-US03350.
 PR 18-FEB-1998; 98US-0025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PI Yeaman MR, Shen AJ;
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 against bacteria and fungi -
 PS Disclosure; Page 59; 166pp; English.
 CC The present invention describes an antimicrobial peptide (AP) for direct
 activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBBZXBXB and BBZXBXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXBX, XBBXXBXB, BXBBXXB, XBBZXBB, and
 CC XBBZXBBXZBBX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid; and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.
 XX
 CC
 SQ Sequence 19 AA;
 Query Match 76.8%; Score 53; DB 20; Length 19;
 Best Local Similarity 84.6%; Pred. No. 0.2;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKMKKLKLS 13
 DB 1 ALYKKMKKLKLS 13
 RESULT 7
 AAY57502
 ID AAY57502 standard; Peptide; 20 AA.
 AC AAY57502;
 XX
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide 0C, 19C-RP-1 SEQ ID NO:40.
 XX
 DE Antimicrobial peptide 0C, 19C-RP-1 SEQ ID NO:40.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 PN WO9942119-A1.
 PD 26-AUG-1999.
 PF 17-FEB-1999; 99WO-US03350.
 PR 18-FEB-1998; 98US-0025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PI Yeaman MR, Shen AJ;
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 against bacteria and fungi -
 PS Disclosure; Page 59; 166pp; English.
 CC The present invention describes an antimicrobial peptide (AP) for direct
 activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBBZXBXB and BBZXBXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXBX, XBBXXBXB, BXBBXXB, XBBZXBB, and
 CC XBBZXBBXZBBX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid; and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.
 XX
 CC
 SQ Sequence 20 AA;
 Query Match 76.8%; Score 53; DB 20; Length 20;
 Best Local Similarity 84.6%; Pred. No. 0.21;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKMKKLKLS 13
 DB 2 ALYKKMKKLKLS 14
 RESULT 8
 AAY57496
 ID AAY57496 standard; Peptide; 25 AA.
 AC AAY57496;
 XX
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
 XX
 DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 PN WO9942119-A1.
 PD 26-AUG-1999.
 PF 17-FEB-1999; 99WO-US03350.
 PR 18-FEB-1998; 98US-0025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PI Yeaman MR, Shen AJ;
 DR WPI; 1999-527417/44.
 XX

PF 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1998; 98US-0025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PI Yeaman MR, Shen AJ;
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 against bacteria and fungi -
 PS Disclosure; Page 59; 166pp; English.
 CC The present invention describes an antimicrobial peptide (AP) for direct
 activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBBZXBXB and BBZXBXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXBX, XBBXXBXB, BXBBXXB, XBBZXBB, and
 CC XBBZXBBXZBBX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid; and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.
 XX
 CC
 SQ Sequence 20 AA;
 Query Match 76.8%; Score 53; DB 20; Length 20;
 Best Local Similarity 84.6%; Pred. No. 0.21;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKMKKLKLS 13
 DB 2 ALYKKMKKLKLS 14
 RESULT 8
 AAY57496
 ID AAY57496 standard; Peptide; 25 AA.
 AC AAY57496;
 XX
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
 XX
 DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 PN WO9942119-A1.
 PD 26-AUG-1999.
 PF 17-FEB-1999; 99WO-US03350.
 PR 18-FEB-1998; 98US-0025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PI Yeaman MR, Shen AJ;
 DR WPI; 1999-527417/44.
 XX

Query Match	Best Local Similarity	Score 53:	DB 20:	Length 35:
Matches 11:	Conservative	1:	Mismatches	1: Indels 0: Gaps 0
QY	1 ALYKKKKNKLKLS 13 :			
Db	1 ALYKKFKKLKLS 13			
RESULT 10				
AAV57500				
ID	AAV57500 standard; Peptide: 18 AA.			
XX	AAV57500;			
AC				
XX				
DT	25-FEB-2000 (first entry)			
XX				
DE	Antimicrobial peptide 13C-RP-1 SRQ ID NO:38.			
XX				
KW	Antimicrobial: metapeptide; PMP-2; platelet microbicidal protein;			
XX	antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.			
OS	Synthetic.			
XX	Oryctolagus cuniculus.			
PN	W09942119-A1.			
XX				
PD	26-AUG-1999.			
XX				
PF	17-FEB-1999; 99WO-US03350.			
XX				
PR	18-FEB-1998; 98US-0025319.			
XX				
PA	(HARB-) HARBOR-UCLA RES & EDUCATION INST.			
XX				
P1	Yeaman MR, Shen AJ;			
DR	WPI: 1999-527417/44.			
XX				
PT	Antimicrobial peptides for potentiating antimicrobial agents active			
XX	against bacteria and fungi -			
PS	Disclosure: Page 58; 16pp; English.			
CC				
CC	The present invention describes an antimicrobial peptide (AP) for direct			
CC	activity or for potentiating antimicrobial agents active against			
CC	organisms such as bacteria and fungi. The AP comprises: (a) a peptide			
CC	containing an amino acid sequence selected from the group consisting			
CC	essentially of a first peptide template XZBXBXB and its derivatives			
CC	selected from XZBXBXBXB, BXZXB, BXZXZXB, XBXZXBXB and BZXZBXZ; and			
CC	(b) a second peptide template XBBXX and their derivatives selected from			
CC	the group consisting of XBBXBBX, XBBXBBX, BXXBXXB, XBBZXBB, and			
CC	XBBZXBBXZBBX; where B = at least one positively charged amino acid;			
CC	X = at least one non-polar hydrophobic amino acid; Z = at least one			
CC	aromatic amino acid, and where B, X and Z may be separated by one or			
CC	more other amino acids. The peptides can be used to treat bacterial and			
CC	fungal infections. The peptides also increase the antimicrobial activity			
CC	of neutrophils. The peptides overall effect cellular disruption and			
CC	rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent			
CC	sequences used in the exemplification of the present invention.			
XX				

CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 18 AA;

Query Match 71.0%; Score 49; DB 20; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.75;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKRNKLK 12
 |||||:| ||||
 DB 1 ALYKKRNKLK 12

RESULT 11
 ID AAY57504 standard; Peptide: 18 AA.

XX AAY57504;

DF 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-1-10F SEQ ID NO:42.

XX Antimicrobial; metapeptide: PMP-2; platelet microbicidal protein;

KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03350.

XX 18-FEB-1998; 98US-0025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi

PS Disclosure; Page 59; 16pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXBXB and its derivatives selected from XBZBXBXB, BXZXB, BXZXXB, XBZXXBXB and BXZBXBXZ; and (b) a second peptide template XBXX and their derivatives selected from the group consisting of XBXXBX, XBXXBXB, BXXBXB, XBZXXB, and XBZXXBXBXZ; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.

SQ Sequence 18 AA;

Query Match 71.0%; Score 49; DB 20; Length 18;

Best Local Similarity 76.9%; Pred. No. 0.75;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKRNKLK 13
 |||||:| ||||

DB 1 ALYKKRNKLK 13

RESULT 12

ID AAY57468 standard; Peptide: 13 AA.

XX AAY57468;

DF 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-4 SEQ ID NO:6.

XX Antimicrobial; metapeptide: PMP-2; platelet microbicidal protein;

KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03350.

XX 18-FEB-1998; 98US-0025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi

PS Disclosure; Page 108; 16pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXBXB and its derivatives selected from XBZBXBXB, BXZXB, BXZXXB, XBZXXBXB and BXZBXBXZ; and (b) a second peptide template XBXX and their derivatives selected from the group consisting of XBXXBX, XBXXBXB, BXXBXB, XBZXXB, and XBZXXBXBXZ; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.

SQ Sequence 13 AA;

Query Match 69.6%; Score 48; DB 20; Length 13;

Best Local Similarity 69.2%; Pred. No. 0.77;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKRNKLK 13
 |||||:| ||||

DB 1 ARYKRNKLK 13

RESULT 13

ID AAY57467 standard; Peptide: 14 AA.

XX AAY57467;

DF 25-FEB-2000 (first entry)

```

XX DE Antimicrobial peptide RP-3 SEQ ID NO:5.
XX XX
XX XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX XX
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX XX
XX PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US03350.
XX PR 18-FEB-1998; 98US-0025319.
XX PS (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI: 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active
XX PT against bacteria and fungi
XX PS Disclosure: Page 108; 166pp: English.
XX CC
XX CC The present invention describes an antimicrobial peptide (AP) for direct
XX CC activity or for potentiating antimicrobial agents active against
XX CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX CC containing an amino acid sequence selected from the group consisting
XX CC essentially of a first peptide template XZBZBXXB and its derivatives
XX CC selected from XZBZBXXBX, BXZXB, BXZXZXB, XBBZXBBX and BBXZBXXZ; and
XX CC (b) a second peptide template XBBXX and their derivatives selected from
XX CC the group consisting of XBBXXBX, XBBXXBBX, BXXBBX, XBBZXXBB, and
XX CC XBBZXXBBXXZBBX; where B = at least one positively charged amino acid;
XX CC aromatic amino acid, and where B, X and Z may be separated by one or
XX CC more other amino acids. The peptides also can be used to treat bacterial
XX CC and fungal infections. The peptides also increase the antimicrobial activity
XX CC of neutrophils. The peptides overall effect cellular disruption and
XX CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
XX CC sequences used in the exemplification of the present invention.
XX CC
XX SQ Sequence 14 AA:
XX
XX Query Match 69.6%; Score 48; DB 20; Length 14;
XX Best Local Similarity 81.8%; Pred. No. 0.82;
XX Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 2 LYKKKMKLKLK 12
DB 2 LYKKKMKLKLK 12
||:|||||
RESULT 14
AAY57466
ID AAY57466 standard; Peptide: 13 AA.
XX
XX AC AAY57466;
XX XX
XX DE 25-FEB-2000 (first entry)
XX XX Antimicrobial peptide RP-2 SEQ ID NO:4.
XX XX
XX KM Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX XX
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX PI

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XX XX
XX PD 26-AUG-1999.
XX XX
XX PF 17-FEB-1999; 99WO-US03350.
XX PR 18-FEB-1998; 98US-0025319.
XX PS (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI: 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active
XX PT against bacteria and fungi
XX PS Disclosure: Page 107; 166pp: English.
XX CC
XX CC The present invention describes an antimicrobial peptide (AP) for direct
XX CC activity or for potentiating antimicrobial agents active against
XX CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX CC containing an amino acid sequence selected from the group consisting
XX CC essentially of a first peptide template XZBZBXXB and its derivatives
XX CC selected from XZBZBXXBX, BXZXB, BXZXZXB, XBBZXBBX and BBXZBXXZ; and
XX CC (b) a second peptide template XBBXX and their derivatives selected from
XX CC the group consisting of XBBXXBX, XBBXXBBX, BXXBBX, XBBZXXBB, and
XX CC XBBZXXBBXXZBBX; where B = at least one positively charged amino acid;
XX CC aromatic amino acid, and where B, X and Z may be separated by one or
XX CC more other amino acids. The peptides also can be used to treat bacterial
XX CC and fungal infections. The peptides also increase the antimicrobial activity
XX CC of neutrophils. The peptides overall effect cellular disruption and
XX CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
XX CC sequences used in the exemplification of the present invention.
XX CC
XX SQ Sequence 13 AA:
XX
XX Query Match 68.1%; Score 47; DB 20; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 1.1;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 ALYKKMKLKLKS 13
DB 1 ARYKKFKKLKLKS 13
|||:|||||
RESULT 15
AAY57503
ID AAY57503 standard; Peptide: 18 AA.
XX
XX AC AAY57503;
XX XX
XX DE 25-FEB-2000 (first entry)
XX XX Antimicrobial peptide RP-1-2R SEQ ID NO:41.
XX XX
XX KM Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX XX
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX XX
XX PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US03350.
XX PR 18-FEB-1998; 98US-0025319.
XX PS (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;

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XX
DR WPI; 1999-527417/44.

XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi

PS Disclosure; Page 59; 166pp; English.

XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZBXXB and its derivatives
CC selected from XZBZBXXB, BXZXB, BXZXXB, XBBZBXXB and BBZBXXZ; and
CC (b) a second peptide template XBBXX and their derivatives selected from
CC the group consisting of XBBXXB, XBBXXBB, BXBBXB, XBBZXXBB, and
CC XBBZXXBBXZBXX; where B = at least one positively charged amino acid;
CC X = at least one non-polar hydrophobic amino acid; Z = at least one
CC aromatic amino acid, and where B, X and Z may be separated by one or
CC more other amino acids. The peptides can be used to treat bacterial and
CC fungal infections. The peptides also increase the antimicrobial activity
CC of neutrophils. The peptides overall effect cellular disruption and
CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
CC sequences used in the exemplification of the present invention.

XX
SQ Sequence 18 AA;

Query Match 68.1%; Score 47; DB 20; Length 18;

Best Local Similarity 76.9%; Pred. No. 1.5;

Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKKKKKLLKS 13

Db 1 ARYKKKKKKLLKS 13

Search completed: December 30, 2002, 16:22:09
Job time : 35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:21:13 ; Search time 16 Seconds

(without alignments)
78.109 Million cell updates/sec

Title: US-09-648-816b-9

Perfect score: 69

Sequence: 1 ALYKKKKMLKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	71.0	445	2	C71636
2	44	63.8	827	2	F96647
3	43	62.3	445	2	G97846
4	42	60.9	245	2	A12126
5	42	60.9	397	2	S62579
6	42	60.9	579	2	B84956
7	41	59.4	286	2	D90609
8	41	59.4	531	2	T41151
9	40	58.0	87	2	AH1445
10	40	58.0	137	1	A36933
11	40	58.0	170	2	AC3409
12	40	58.0	175	2	E82941
13	40	58.0	361	2	AC1437
14	40	58.0	453	2	H81151
15	39	56.5	453	2	D81870
16	39	56.5	119	2	D98013
17	39	56.5	162	2	A82911
18	39	56.5	277	2	H86589
19	39	56.5	277	2	C72033
20	39	56.5	338	2	T39635
21	39	56.5	342	2	T43038
22	39	56.5	439	2	T28196
23	39	56.5	487	2	S11886
24	39	56.5	492	2	S11885
25	39	56.5	528	4	S11887
26	39	56.5	569	2	S11885
27	39	56.5	569	2	E90554
28	39	56.5	660	2	S40098
29	39	56.5	759	2	T43031

30	39	56.5	838	2	T40750	hypothetical prote
31	39	56.5	1048	2	S64758	SCD25 protein (ver
32	39	56.5	1250	2	S14177	SCD25 protein (ver
33	38.5	55.8	628	2	AT2393	hypothetical prote
34	38	55.1	117	2	T44090	15150-like transpo
35	38	55.1	118	2	H81143	hypothetical prote
36	38	55.1	180	2	B64353	hypothetical prote
37	38	55.1	185	2	B64394	hypothetical prote
38	38	55.1	293	1	OOCV8V	Bil protein - squa
39	38	55.1	439	2	B86302	hypothetical prote
40	38	55.1	453	2	F81720	lipid A biosynthes
41	38	55.1	455	2	E71569	probable acyltrans
42	38	55.1	520	2	T49478	probable glutamate
43	38	55.1	896	2	I56563	interleukin-3 rece
44	38	55.1	967	2	S58360	antibiotic Pep5 D
45	38	55.1	969	2	S17909	hypothetical prote

ALIGNMENTS

RESULT 1

C71636

probable thiophene and furan oxidation protein thdf (thdf) RP759 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #textl_change 02-Feb-2001

C:Accession: C71636

R.Andersson, S.G.F.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark

Nature 396, 135-140, 1998

A>Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; PMID:99039499; PMID:9823893

A:Accession: C71636

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-445 <AMD>

A:Cross-references: GB:A7235273; GB:A7235269; NID:93861237; PIDN:CAAL5187.1; PID:9386

A:Experimental source: strain Madrid E

A:Genetics:

A:Gene: thdf; RP759

C:Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu h

C:Keywords: GTP binding; nucleotide binding; P-loop

F:216-332/Domain: translation elongation factor Tu homology <ETU>

F:222-229/Region: nucleotide-binding motif A (P-loop)

F:329-332/Region: GTP-binding NKXD motif

Query Match

Best Local Similarity 71.0%; Score 49; DB 2; Length 445;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYKKKKMLK 12

Db 154 LYKKKKNDLKR 164

RESULT 2

F96647

hypothetical protein F19K23.6 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #textl_change 31-Mar-2001

C:Accession: F96647

R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; PMID:21016719; PMID:11130712

A:Accession: F96647

A>Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-827 <STO>
 A:Cross-references: GB:AE005173; NID:g2160138; PIDN:AA60760.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F19K23.6
 A:Map position: 1

Query Match 63.8%; Score 44; DB 2; Length 827;
 Best Local Similarity 61.5%; Pred. No. 26;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKKWKNNKLK 13
 ||:|||||
 Db 282 AMKKWPNILTKS 294

RESULT 3
 G97846
 hypothetical protein thdf [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
 C:Accession: G97846
 R:Orgat, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
 Science 293, 2093-2098, 2001
 A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: G97846
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-445 <KUR>
 A:Cross-references: GB:AE006914; PIDN:AL03713.1; PID:g15620303; GSPDB:GN00173
 C:Genetics:
 A:Gene: thdf
 C:Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu hom

Query Match 62.3%; Score 43; DB 2; Length 445;
 Best Local Similarity 58.3%; Pred. No. 21;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKWKNNKLK 12
 ||| |::|||
 Db 153 ALYNNMRSQILK 164

RESULT 4

AI2126
 hypothetical protein all2568 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AI2126

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iritaghi
 Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AI2126
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-245 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA74267.1; PID:g17131660; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:

A:Gene: all2568
 C:Superfamily: Synechocystis hypothetical protein slr1718

Query Match 60.9%; Score 42; DB 2; Length 245;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKWKNNKLK 11
 ||| |::||
 Db 189 ALYSQWNNLL 199

RESULT 5
 S62579
 Probable plasma membrane iron permease - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000
 C:Accession: S62579; T38101
 R:Murphy, L.; Niblett, D.; Harris, D.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: S62573

A:Accession: S62579
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-397 <MUR>
 A:Cross-references: EMBL:Z67998; NID:g1067202; PIDN:CAA91954.1; PID:g1067209
 R:Beck, A.; Reinhardt, R.; Murphy, L.; Niblett, D.; Harris, D.; Barrell, B.G.; Rajand
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z21769
 A:Accession: T38101

A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-397 <MUR>
 A:Cross-references: EMBL:Z67998; NID:g1067202; PIDN:CAA91954.1; GSPDB:GN00066; SPDB:S
 A:Experimental source: strain 972h; cosmid clF7
 C:Genetics:
 A:Gene: SPAC17.07c
 A:Map position: 1R
 C:Superfamily: conserved probable membrane protein YBR207w

Query Match 60.9%; Score 42; DB 2; Length 397;
 Best Local Similarity 58.3%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 LYKKWKNNKLK 13
 |::|||::|||
 Db 118 LOEKWKNNKLK 129

RESULT 6

B84956
 cell division protein ftsI [imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: B84956
 R:Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
 Nature 407, 81-86, 2000
 A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
 A:Reference number: A84930; MUID:20445173; PMID:10993077

A:Accession: B84956
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-579 <STO>
 A:Cross-references: GB:AP000398; GSPDB:GN00144
 A:Experimental source: strain APS
 C:Genetics:
 A:Gene: ftsI; BU222
 C:Superfamily: penicillin-binding protein 3

Query Match 60.9%; Score 42; DB 2; Length 579;
 Best Local Similarity 66.7%; Pred. No. 39;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 LYKKWKNNKLK 13
 |||||::|||
 Db 1 MYKKKNNKLK 12

RESULT 7

D9609
 conserved hypothetical protein MYPU_7800 [imported] - Mycoplasma pulmonis (strain UAB
 C:Species: Mycoplasma pulmonis
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: E82941
 R:Glass, J.J.; Lefkowitz, E.J.; Glass, J.S.; Helner, C.R.; Chen, E.Y.; Cassell, G.H.
 Submitted to GenBank, February 2000
 A:Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a mit
 A:Reference number: A82870
 A:Accession: E82941
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-175 <GLA>
 A:Cross-references: GB:AE002103; GB:AF222894; NID:g6898977; PIDN:AAF30437.1; GSPDB:GN001
 A:Experimental source: serovar 3; biovar 1
 C:Genetics:
 A:Gene: UU032
 A:Genetic code: SGC3

Query Match 58.0%; Score 40; DB 2; Length 175;
 Best Local Similarity 75.0%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKRNK 9
 :|||
 Db 70 VYKWKMK 77

RESULT 13
 AC1437
 Glucosamine-fructose-6-phosphate aminotransferase (C-terminal domain) homolog lin0034 [A
 C:Species: *Listeria innocua*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AC1437
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioeche
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schleuter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A:Title: Comparative genomics of *Listeria* species
 A:Reference number: AB1077; MUID:21357279; PMID:11679669
 A:Accession: AC1437
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361 <GLA>
 A:Cross-references: GB:AL592022; PIDN:GAC95267.1; PID:g16412455; GSPDB:GN00178
 A:Experimental source: strain C11p11262
 C:Genetics:
 A:Gene: lin0034

Query Match 58.0%; Score 40; DB 2; Length 361;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKKRNK 9
 :|||
 Db 200 AFYEKKME 208

RESULT 14
 H81151
 POLYA polymerase NMB0843 [imported] - *Neisseria meningitidis* (strain MC58 serogroup B)
 C:Species: *Neisseria meningitidis*
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: H81151
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.R.; Haft, D.R.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: AB1000; MUID:20175755; PMID:10710307
 A:Accession: H81151
 A>Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-453 <TE>
 A:Cross-references: GB:AE002437; GB:AE002098; NID:g7226072; PIDN:AAF41254.1; PID:g722
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB0843

Query Match 58.0%; Score 40; DB 2; Length 453;
 Best Local Similarity 58.3%; Pred. No. 65;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKRNKMLKS 13
 :|||
 Db 1 MLKKWLNMKMLPS 12

RESULT 15
 D81870
 Probable polynucleotide adenyllyltransferase (EC 2.7.7.19) NMA1053 [imported] - *Neisse*
 C:Species: *Neisseria meningitidis*
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: D81870
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491
 A:Reference number: AB1775; MUID:20222556; PMID:10761919
 A:Accession: D81870
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-453 <PAR>
 A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84318.1; PID:g737
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: pcmb; NMA1053
 C:Keywords: nucleotidyltransferase

Query Match 58.0%; Score 40; DB 2; Length 453;
 Best Local Similarity 58.3%; Pred. No. 65;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKRNKMLKS 13
 :|||
 Db 1 MLKKWLNMKMLPS 12

Search completed: December 30, 2002, 16:23:26
 Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:18:28 : Search time 11 Seconds

(without alignments)
49.017 Million cell updates/sec

Title: US-09-648-816b-9
Perfect score: 69
Sequence: 1 ALYKKMKKLKS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	71.0	445	1 TRME_RICPR	092c11 rickettsia
2	43	62.3	445	1 TRME_RICCN	092ge8 rickettsia
3	42	60.9	245	1 COMB_ANASP	08yrt5 anabena sp
4	42	60.9	397	1 YAK7_SCHPO	009919 schizosacch
5	42	60.9	579	1 FTSI_BUCAL	p57317 buchnera ap
6	42	60.9	1971	1 MC3A_MOUSE	094uu9 mus musculu
7	40	58.0	137	1 KQGL_STRMU	006888 streptococc
8	40	58.0	175	1 Y032_UREPA	096rb3 ureaplasma
9	39	56.5	293	1 VBL1_BGMV	006001 bean golden
10	39	56.5	569	1 SYE_TOBAC	043794 nicotiana t
11	39	56.5	759	1 TOP3_CAEEL	061660 caenorhabdi
12	39	56.5	1215	1 BGCN_DROME	094112 drosophila
13	39	56.5	1253	1 SC25_YEAST	p14771 saccharomyc
14	38	55.1	180	1 Y426_METJA	051869 methanococc
15	38	55.1	185	1 Y754_METJA	058164 methanococc
16	38	55.1	252	1 ORC6_HUMAN	094516 homo sapien
17	38	55.1	262	1 ORC6_MOUSE	094u18 mus musculu
18	38	55.1	293	1 VBL1_SLICV	p21936 squash leaf
19	38	55.1	969	1 DPOM_NEUTN	p33538 neurospora
20	38	55.1	2514	1 POLN_STINDO	p21283 sandbis vir
21	37	53.6	90	1 PLF4_PIG	p30034 sus scrofa
22	37	53.6	130	1 YGHS_YEAST	p33199 saccharomyc
23	37	53.6	249	1 MCT1_CANPA	p21842 canis famli
24	37	53.6	264	1 MEZ4_SCHPO	096ws1 schizosacch
25	37	53.6	347	1 Y9I_YEAST	p41172 saccharomyc
26	37	53.6	377	1 Y412_MYCE	p41652 mycoplasma
27	37	53.6	473	1 MWIN_THERMA	094xul thermotoga
28	37	53.6	645	1 REP_BUCAL	p57654 buchnera ap
29	37	53.6	785	1 PTAL_YEAST	001329 saccharomyc
30	37	53.6	792	1 SYL_MYCE	p47508 mycoplasma
31	37	53.6	878	1 IL3B_MOUSE	p26954 mus musculu
32	37	53.6	896	1 CYRB_MOUSE	p26955 mus musculu
33	37	53.6	1068	1 YCF0_MARPO	p12221 marichantia

34	37	53.6	1097	1 KPCL_CANAL	P43057 candida alb
35	37	53.6	3088	1 POLG_PEWVC	001500 p genome po
36	36.5	52.9	370	1 YG2G_YEAST	p53249 saccharomyc
37	36.5	52.9	500	1 XYNB_THESJ	030360 thermoaer
38	36	52.2	83	1 RPOR_SULAC	p39463 sulfobus
39	36	52.2	83	1 Y019_BACAN	091n13 bacterioph
40	36	52.2	137	1 UVSY_BPT4	p04537 bacterioph
41	36	52.2	171	1 VGS6_BPT4	p39262 bacterioph
42	36	52.2	206	1 YMB0_YEAST	004019 saccharomyc
43	36	52.2	214	1 ST21_RAT	P09005 rattus norv
44	36	52.2	241	1 COMB_SYNY3	p73849 synecocyst
45	36	52.2	247	1 EDIN_STAAU	P24121 staphylococ

ALIGNMENTS

RESULT 1
ID TRME_RICPR STANDARD: PRT: 445 AA.
AC 092C11:
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable trna modification GTPase trme.
GN TRME OR THDF OR RP759.
OS Rickettsia prowazekii.
OC Bacteria: Proteobacteria; alpha subdivision: Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_Taxid=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E.
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,
RA Slicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
mitochondria".
RL Nature 396:133-140(1998).
CC -I- INVOLVED IN THE BIOSYNTHESIS OF THE HYPERMODIFIED NUCLEOSIDE 5-
METHYLAMINOMETHYL-2-THIOURIDINE, WHICH IS FOUND IN THE WOBBLE
POSITION OF SOME TRNAS (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING
PROTEINS. TRME SUBFAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ235273; CAA15187.1; -
DR InterPro: IPR005289; GTP-binding_dom.
DR InterPro: IPR002917; MMR_HSR1.
DR InterPro: IPR005225; Small_GTP.
DR InterPro: IPR004520; ThdF.
DR Pfam: PF01926; MMR_HSR1.1.
DR TIGRFAMs: TIGR00231; small_GTP.1.
DR TIGRFAMs: TIGR00450; thdF.1.
DR TIGRFAMs: TIGR00650; MG442.1.
KM trna processing; GTP-binding; Complete proteome.
FT NP_BIND 222 229 GTP (POTENTIAL).
FT NP_BIND 269 273 GTP (POTENTIAL).
FT NP_BIND 329 332 GTP (POTENTIAL).
SQ SEQUENCE 445 AA; 49813 MW; FA158F99E716B4F6 CRC64;
Query Match 71.0%; Score 49; DB 1; Length 445;
Best Local Similarity 72.7%; Pred. No. 0.98;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

OY      2 LYKKWKNNKLLK 12
      111111111
Db      154 LYNNKRNQLLK 164

RESULT 2
TRME_RICCN      STANDARD:      PRT:      445 AA.
ID TRME_RICCN
AC 09ZGE8:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE tRNA modification GTPase trme.
GN TRME OR THDF OR RC1175.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
  Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
  Sanson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
  Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
  Science 293:2093-2098(2001).
CC -1- FUNCTION: Exhibits a very high intrinsic GTPase hydrolysis rate.
  Involved in the biosynthesis of the hypermodified nucleoside 5-
  methylaminomethyl-2-thiouridine, which is found in the wobble
  position of some tRNAs (by similarity).
CC -1- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING
  PROTEINS. TRME SUBFAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE008665; ALU03713.1;
DR InterPro: IPR005289; GTP-binding_dom.
DR InterPro: IPR002917; MMR_HSR1.
DR InterPro: IPR005225; Small_GTP.
DR InterPro: IPR004520; ThdF.
DR Pfam: PF01926; MMR_HSR1.1.
DR TIGRFAMs: TIGR00650; MG442.1.
DR TIGRFAMs: TIGR00231; small_GTP.1.
DR TIGRFAMs: TIGR00450; thdF.1.
KW tRNA processing; GTP-binding; Complete proteome.
FT NP_BIND 222 229 GTP (POTENTIAL).
FT NP_BIND 269 273 GTP (POTENTIAL).
FT NP_BIND 329 332 GTP (POTENTIAL).
SQ SEQUENCE 445 AA; 49399 MW; 58F4BDE2D1CDAE64 CRC64;

Query Match 62.3%; Score 43; DB 1; Length 445;
Best Local Similarity 58.3%; Pred. NO. 9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable 2-phosphosulfolactate phosphatase (EC 3.1.3.-).
GN COMB OR ALI2568
OS Anabaena sp. (Strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
  Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
  Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
  Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
  Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
  cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
CC -1- CATALYTIC ACTIVITY: 2-phosphosulfolactate = sulfolactate +
  phosphate.
CC -1- COFACTOR: Magnesium (by similarity).
CC -1- SIMILARITY: BELONGS TO THE COMB FAMILY.
CC -----
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  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AP003589; BAB74267.1;
DR InterPro: IPR005238; 2-ph-phosphatase.
DR TIGRFAMs: TIGR00298; TIGR00298.1.
KW Hydrolyase; Magnesium; Complete proteome.
SQ SEQUENCE 245 AA; 26694 MW; BC7F4BBAE5B6958 CRC64;

Query Match 60.9%; Score 42; DB 1; Length 245;
Best Local Similarity 63.6%; Pred. NO. 7.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OY      1 ALYKKWKNNKLLK 12
      111111111
Db      153 ALYNNRNSQLLK 164

RESULT 3
COMB_ANASP      STANDARD:      PRT:      245 AA.
AC 08Y25:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)

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DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable 2-phosphosulfolactate phosphatase (EC 3.1.3.-).
GN COMB OR ALI2568
OS Anabaena sp. (Strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
  Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
  Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
  Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,
  Gentles S., Goble A., Hamlin N., Harris P., Hildalgo J., Hodgson G.,
  Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
  James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
  Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
  Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
  Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

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RA Skelton J., Stimmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Wolckart G., Aert R., Robben J., Grymonprez B.,
 RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purrelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motlier S.,
 RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garçon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Usero D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE FTFL FAMILY.
 CC -----
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 CC -----
 CC EMBL: Z67998; CAA91954.1; -
 DR InterPro: IPR004923; FTFL.
 DR Pfam: PF03239; FTFL1.1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 92 112 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT TRANSMEM 292 312 POTENTIAL.
 SQ SEQUENCE 397 AA: 44314 MW: 1D98EA1AD1FD708F CRC64:
 Query Match 60.9%; Score 42; DB 1; Length 397;
 Best Local Similarity 58.3%; Pred. No. 12;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LYKKNKRLKLS 13
 Db 118 LDEKMKRLKLS 129
 RESULT 5
 FTSL_BUCAI
 ID FTSL_BUCAI STANDARD: PRT: 579 AA.
 AC P57317.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidoglycan synthetase ftsI (Penicillin-binding protein 3) (PBP-3).
 GN FTSI OR B0222.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1996;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RL Buchnera sp. Aps.";
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: CELL WALL FORMATION. ESSENTIAL FOR THE FORMATION OF A
 CC SEPTUM OF THE MOREIN SACCULUS. SYNTHESIS OF CROSS-LINKED
 CC PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES (BY SIMILARITY).
 CC -1- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
 CC -1- DOMAIN: HAS AN N-TERMINAL PENICILLIN INSENSITIVE TRANSGLYCOSYLASE

CC DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) & A CARBOXY-TERMINAL
 CC PENICILLIN-SENSITIVE TRANSEPTIDASE DOMAIN (CROSS-LINKING OF THE
 CC PEPTIDE SUBUNIT).
 CC -1- SIMILARITY: BELONGS TO THE TRANSEPTIDASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: AP001118; BAB12938.1; -
 DR InterPro: IPR005311; PBP_dimer.
 DR InterPro: IPR001460; Transpeptidase.
 DR Pfam: PF00905; Transpeptidase; 1.
 DR Pfam: PF03717; PBP_dimer; 1.
 KW Transmembrane; peptidoglycan synthesis; Cell division; Cell wall;
 KW Multifunctional enzyme; Cell shape; Complete proteome.
 FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 22 42 POTENTIAL.
 FT DOMAIN 43 579 EXTRACELLULAR (POTENTIAL).
 FT ACT_SITE 305 305 ACYLATED BY PENICILLIN (BY SIMILARITY).
 SQ SEQUENCE 579 AA: 65204 MW: E3717820808CAD12 CRC64:
 Query Match 60.9%; Score 42; DB 1; Length 579;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LYKKNKRLKLS 13
 Db 1 MYKKEKNRFLKS 12
 RESULT 6
 MCM3_MOUSE
 ID MCM3_MOUSE STANDARD: PRT: 1971 AA.
 AC O9WU9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 80 kDa MCM3-associated protein (GAMP protein).
 GN MCM3AP OR GAMP OR MAP80.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C X NZB;
 RX MEDLINE=20197882; PubMed=10733502;
 RA Kuwahara K., Yoshida M., Kondo E., Sakata A., Watanabe Y., Abe E.,
 RA Kondo Y., Tomiyasu S., Fujimura S., Tokuhisa T., Kimura H., Ezaki T.,
 RA Sakaguchi N.;
 RT "A novel nuclear phosphoprotein, GAMP, is up-regulated in centrocytes
 RT of the germinal center and associated with MCM3, a protein essential
 RT for DNA replication.";
 RL Blood 95:2321-2328(2000).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE NUCLEAR LOCALIZATION PATHWAY OF
 CC MCM3 (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH MCM3.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- PTM: PHOSPHORYLATED (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE SAC3 FAMILY.
 CC -----
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 CC -----

CC -----
 DR EMBL: AJ006590; CAB4241.1; -
 DR MGI: 1930089; Mgm3ap.
 DR InterPro: IPR005062; SAC3_GANP.
 DR Pfam: PF03399; SAC3_GANP; 1.
 DR Nuclear protein; Phosphorylation.
 SO SEQUENCE 1971 AA; 217138 MW; 5F342E256C007E24 CRC64;

Query Match 60.9%; Score 42; DB 1; Length 1971;
 Best Local Similarity 77.8%; Pred. No. 53;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 YKKWKMKLL 11
 1:||||| 1
 Db 1710 YKKWKMKSL 1718

RESULT 7

KDGL_STRMU STANDARD; PRT; 137 AA.
 ID KDGL_STRMU
 AC Q05888; 051807; (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Diacylglycerol kinase (EC 2.7.1.107) (DAGK) (Diacylceride kinase) (DGK).
 GN DGK OR DGK.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 CC Streptococcus.
 OX NCBI_TaxID=1309;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=GS-5;
 RX MEDLINE=94012483; PubMed=8407794;
 RA Yamashta Y., Takehara T., Kuramitsu H.K.;
 RT "Molecular characterization of a Streptococcus mutans mutant altered in environmental stress responses.";
 RL J. Bacteriol. 175:6220-6228(1993).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=T8;
 RX MEDLINE=98083071; PubMed=9422608;
 RA Chen P., Novak J., Qi F.-Q., Caulfield P.W.;
 RT "Diacylglycerol kinase is involved in regulation of expression of the lactobiotic mutacin II of Streptococcus mutans.";
 RL J. Bacteriol. 180:167-170(1998).
 CC -1- FUNCTION: RECYCLING OF DIACYLGLYCEROL PRODUCED DURING THE TURNOVER OF MEMBRANE PHOSPHOLIPID. MAY PLAY A ROLE IN ADAPTABILITY TO ENVIRONMENTAL STRESS CONDITIONS SUCH AS ACID TOLERANCE, ELEVATED TEMPERATURES AND HIGH OSMOLARITY.
 CC -1- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-diacylglycerol 3-phosphate.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL DIACYLGLYCEROL KINASE FAMILY.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
 CC -----
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 CC -----
 CC EMBL: L12211; AAA26867.1; -
 DR EMBL: AF000954; AAC38047.1; -
 DR InterPro: IPR000829; DAGK_prokar.
 DR Pfam: PF01219; DAGK_prokar; 1.
 DR Prodom: P0010722; DAGK_prokar; 1.
 DR PROSITE: PS01069; DAGK_PROKAR; 1.
 DR Phospholipid biosynthesis; Transferase; Kinase; Transmembrane.
 KW DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 FT

FT TRANSMEM 43 58 POTENTIAL.
 FT TRANSMEM 62 78 POTENTIAL.
 FT DOMAIN 79 108 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 109 129 POTENTIAL.
 FT CONFLICT 128 129 LL -> VP (IN REF. 2).
 SO SEQUENCE 137 AA; 15380 MW; 4F01654885319125 CRC64;

Query Match 58.0%; Score 40; DB 1; Length 137;
 Best Local Similarity 70.0%; Pred. No. 9;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 KKKWKMLKS 13
 1:||||| 1
 Db 13 KKKWKMLTSS 22

RESULT 8

Y032_UREPA STANDARD; PRT; 175 AA.
 ID Y032_UREPA
 AC Q9PRB3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein U0032.
 GN U0032.
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
 OX NCBI_TaxID=134821;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sevovar 3;
 RX MEDLINE=20500219; PubMed=11048724;
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Helner C.R., Chen E.Y., Cassell G.H.;
 RT "The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";
 RL Nature 407:757-762(2000).
 CC -----
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 CC -----
 CC EMBL: AE002103; AAF30437.1; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 175 AA; 20950 MW; 93FDAD28712E5222 CRC64;
 Query Match 58.0%; Score 40; DB 1; Length 175;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYKKWKNK 9
 1:||||| 1
 Db 70 LYKKWKNK 77

RESULT 9

VBL1_BGMV STANDARD; PRT; 293 AA.
 ID VBL1_BGMV
 AC P06001;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE B11 protein (33.1 kDa protein).
 GN BCL1.
 OS Bean golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10839;
 RN 11
 RP SEQUENCE FROM N.A.
 FT

RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
 RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
 RL regulation in geminiviruses";
 CC Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES BL1 PROTEIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: M10080; AAA46323.1; -
 DR InterPro: IPR000211; Gemini.B1.
 DR Pfam: PF00845; Gemini.B1; 1
 SO SEQUENCE 293 AA; 33099 MW; CC3C4E0E93A79441 CRC64;

Query Match
 Best Local Similarity 56.5%; Score 39; DB 1; Length 293;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 YKKKKKKLKS 13
 Db 178 YKKKKKKLKS 188

RESULT 10
 ID SVE_TOBAC STANDARD; PRT; 569 AA.
 AC 043794;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
 DE (GLURS)
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 ON NCBI_TaxID=4097;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. SRL; TISSUE=leaf;
 RA Andersen R.V.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) -> AMP +
 CC diphosphate + L-glutamyl-tRNA(Glu).
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X83524; CA58506.1; -
 DR HSSP: P27000; 1GLN.
 DR InterPro: IPR004527; GltX_bact.
 DR InterPro: IPR000924; Glt_rRNA-synt_1c.
 DR InterPro: IPR001412; tRNA-synt_1c.
 DR Pfam: PF00749; tRNA-synt_1c; 1.
 DR PRINTS: PR00987; TRNASYNTGLU.
 DR TIGRFAMs: TIGR00464; gltX_bact. 1.
 DR PROSITE: PS00178; AA_rRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; A-P-binding.
 FT SITE 62 72 "HIGH" REGION.
 FT SITE 303 307 "KMSK" REGION.
 FT BINDING 306 306 ATP (BY SIMILARITY).
 SO SEQUENCE 569 AA; 63338 MW; F2E81D73460A1844 CRC64;

Query Match
 Best Local Similarity 56.5%; Score 39; DB 1; Length 569;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKKKLKS 13
 Db 141 ALYKKKKLKS 153

RESULT 11
 ID TOP3_CAEFL STANDARD; PRT; 759 AA.
 AC 06160; Q90223;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA topoisomerase III (EC 5.99.1.2).
 GN TOP-3 OR Y56A3A.27.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Kim Y.-C., Koo H.-S.;
 RT "cDNA cloning and overexpression of Caenorhabditis elegans DNA
 RT topoisomerase III.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Matthews L.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
 CC DNA, followed by passage and rejoining.
 CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF057032; AAC13567.1; -
 DR EMBL: AL32860; CAB60518.2; -
 DR WormPep: Y56A3A.27; CE28138.
 DR InterPro: IPR002936; DNAPrim_toprim.
 DR InterPro: IPR003601; DNATopI_ATP_bind.
 DR InterPro: IPR003602; DNATopI_DNA_bind.
 DR InterPro: IPR000380; ProK_topisomrase.
 DR Pfam: PF01131; Topoisom_bac; 1.
 DR Pfam: PF01751; Toprim; 1.
 DR PRINTS: PR00417; PRTISMASE1.
 DR SMART: SM00437; TOP1AC; 1.
 DR SMART: SM00436; TOP1BC; 1.
 DR SMART: SM00493; TOPRIM; 1.
 DR PROSITE: PS00396; TOPOISOMERASE_I_PROK; 1.
 KW Isomerase; Topoisomerase; DNA-binding.
 FT ACT_SITE 334 334 DNA_CLEAVAGE (BY SIMILARITY).
 SO SEQUENCE 759 AA; 85438 MW; 3D862412D72946BD CRC64;

Query Match
 Best Local Similarity 56.5%; Score 39; DB 1; Length 759;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYKMKMKL 11
 DB 455 YVEKMGNRML 464

RESULT 12
 BGCN.DROME STANDARD: PRT: 1215 AA.
 ID BGCN.DROME
 AC 09M12: 09M13: 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Benign gonial cell neoplasm protein.
 GN BGCN OR B(2)GCN OR CG30170/CG10331.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 OX NCBI_TaxID=7227;
 RN SEQUENCE FROM N.A.
 RP TISSUE=Testis;
 RC MEDLINE=20384590: PubMed-10924476;
 RX Chlstein B., Iavov C.A., Vef O., Gateff E., McKearin D.M.;
 RT "The Drosophila cystoblast differentiation factor, benign gonial cell
 RT neoplasm, is related to DEXH-box proteins and interacts genetically
 RT with bag-of-marbles."
 RL Genetics 155:1809-1819(2000).
 RN 12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006: PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Arroll J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jatalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skipski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [3]
 RP REVISIONS.

RC STRAIN=Berkley;
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C.M., Berman J.P., Carlson J.W., Celniker S.E.,
 RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
 RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,
 RA Russo S., Seale S.M.J., Smith E., Shu S., Smutnack F.,
 RA Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Mungall C.J., Lewis S.E.; melanogaster genome."
 RT "Annotation of Drosophila melanogaster genome."
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ESSENTIAL CYSTOBLAST DIFFERENTIATION FACTOR REQUIRED FOR
 CC BAM FUNCTION IN ASYMMETRIC DIVISION OF THE GERMLINE STEM CELLS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND IN 5-8 GERMLINE STEM
 CC CELLS OF OVARY. IMMEDIATELY ADJACENT TO TERMINAL FILAMENT.
 CC -1- SIMILARITY: SOME SIMILARITIES TO DEXH-BOX PROTEINS BUT OUTSIDE OF
 CC THE HELICASE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 ANK REPEAT.
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 CC
 CC EMBL: AF255662: AAF91348.1: -
 CC EMBL: AF003462: AAF47077.2: -
 CC Flybase: FBgn004581: dgcn.
 CC InterPro: IPR002110: ANK.
 CC Pfam: PF00023: ank; 2.
 CC SMART: SM00248: ANK; 1.
 CC PROSITE: PS50297: ANK_REPEAT_REGION; 1.
 CC PROSITE: PS50088: ANK_REPEAT; 1.
 CC Developmental protein, ANK repeat.
 CC REPEAT 407 439
 CC SEQUENCE 1215 AA: 139278 MW: 11F83C1B3816F2CD CRC64:
 SQ

Query Match 56.5%; Score 39; DB 1; Length 1215;
 Best Local Similarity 56.6%; Pred. No. 1e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYKMKMKL 10
 DB 792 LYKMGNRML 800

RESULT 13
 SC25.YEAST STANDARD: PRT: 1253 AA.
 ID SC25.YEAST
 AC P14771:
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE SC25 protein.
 GN SC25 OR SDC25 OR YIL016W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M303;
 RX MEDLINE=91094833: PubMed-1986220;
 RA Damek F., Boy-Marcotte E., le Roscouet D., Guibaud R., Jacquet M.;
 RT "SDC25, a CDC25-like gene which contains a RAS-activating domain and
 RT is a dispensable gene of Saccharomyces cerevisiae."
 RL Mol. Cell. Biol. 11:202-212(1991).
 RN [2]
 RP SEQUENCE OF 668-1253 FROM N.A.
 RC STRAIN=01136;
 RX MEDLINE=89306677: PubMed-2545538;

RA Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquet M.;
 RT "The C-terminal part of a gene partially homologous to CDC 25 gene
 suppresses the cdc25-5 mutation in *Saccharomyces cerevisiae*.";
 RL Gene 77:21-30(1989).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=90260633; PubMed=2188363;
 RA Crechet J.B., Poulet P., Mistou M.-Y., Parmegiani A., Camonis J.,
 RA Boy-Marcotte E., Damak F., Jacquet M.;
 RT "Enhancement of the GDP-GTP exchange of RAS proteins by the carboxyl-
 terminal domain of SCD25";
 RL Science 248:866-868(1990).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=91156312; PubMed=2000228;
 RA Rey I., Schweighoffer F., Barlat I., Camonis J., Boy-Marcotte E.,
 RA Guilhard R., Jacquet M., Tocque B.;
 RT "The COOH domain of the product of the *Saccharomyces cerevisiae* SCD25
 gene elicits activation of p21-ras proteins in mammalian cells";
 RL Oncogene 6:347-349(1991).
 CC CC -1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
 CC CC -1- MISCELLANEOUS: SUPPRESSES THE CDC25-5 MUTATION IN YEAST (RESTORES
 CC CC -1- CAMP LEVEL) AND HAS SIMILAR FUNCTIONS AS CDC25.
 CC CC -1- SIMILARITY: CONTAINS 1 RAS-GEP DOMAIN.
 CC CC -1- SIMILARITY: CONTAINS 1 RAS-GEP DOMAIN.
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 CC CC -----
 DR EMBL: M26647; AAA16565.1; -
 DR PIR: S14177; S14177.
 DR SCD: S0003939; SDC25.
 DR InterPro: IPR001895; RasGEF_CDC25.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00617; RasGEF; 1.
 DR Pfam: PF00618; RasGEF; 1.
 DR SMART: SM00147; RasGEF; 1.
 DR SMART: SM00229; RasGEF; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS00720; GDS_CDC25; 1.
 DR PROSITE: PS0002; SH3; 1.
 DR KW Guanine-nucleotide releasing factor; Cell cycle; Cell division;
 KW SH3 domain.
 FT DOMAIN 26 98 SH3.
 FT DOMAIN 74 79 POLY-ASN.
 FT DOMAIN 434 437 POLY-ARG.
 FT VARIANT 584 590 DVVVKFI -> V (IN STRAIN 01136).
 SQ SEQUENCE 1253 AA; 144979 MW; 2DE2C9EC2FE3E60D CRC64;
 Query Match 56.5%; Score 39; DB 1; Length 1253;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 LYKKRNKLKLS 13
 DB 978 LQTKRNKNTKS 989
 RESULT 14
 Y426_METJA STANDARD; PRT; 180 AA.
 AC 057869;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M0426.

GN M0426.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 jannaschii";
 RL Science 273:1058-1073(1996).
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 CC CC -----
 DR EMBL: U67494; AAB98419.1; -
 DR TIGR: M0426; -
 DR KW Hypothetical protein; Complete proteome.
 FT DOMAIN 45 51 POLY-GLU.
 SQ SEQUENCE 180 AA; 21609 MW; E9BE603DEBAE4053 CRC64;
 Query Match 55.1%; Score 38; DB 1; Length 180;
 Best Local Similarity 77.8%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALYKKRNK 9
 DB 101 ALYIDMKNK 109
 RESULT 15
 Y754_METJA STANDARD; PRT; 185 AA.
 AC Q58164;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M0754.
 GN M0754.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 jannaschii";
 RL Science 273:1058-1073(1996).

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CC -----
 CC DR EMBL: D67521; AAB98756.1; -.
 CC TIGR: M70754; -.
 CC KW Hypothetical protein; Complete proteome.
 CC SEQUENCE 185 AA; 21765 MW; 2CE5EC9D424895F6 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 185;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKMKKLLKS 13
 DB 38 LYKKMKLQIFKN 49

Search completed: December 30, 2002, 16:22:28
 Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:20:53 ; Search time 28 seconds
(without alignments)
95.665 Million cell updates/sec

Title: US-09-648-816b-9
Perfect score: 69
Sequence: 1 ALYKKKKKKLLKS 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	DB ID	Description
1	47	68.1	508 16 08R6X0	08R6X0 thermomac
2	44	63.8	215 2 09Z655	09Z655 zymomonas m
3	44	63.8	827 10 004578	004578 arabidopsis
4	43	62.3	1891 12 08Q024	08Q024 sindbis vir
5	43	62.3	2508 12 08Q023	08Q023 sindbis vir
6	42	60.9	293 12 067584	067584 bean golden
7	41	59.4	107 10 09L196	09L196 arabidopsis
8	41	59.4	286 16 09RPE3	09RPE3 mycoplasma
9	41	59.4	307 2 09KH70	09KH70 brevicapilli
10	41	59.4	439 12 08W3P3	08W3P3 swinepox vi
11	41	59.4	531 3 074858	074858 schizosacch
12	41	59.4	762 8 09G872	09G872 rhodomonas
13	40	58.0	87 16 09ZFK1	09ZFK1 listeria in
14	40	58.0	170 16 08TGA3	08TGA3 brucella me
15	40	58.0	259 2 P72185	P72185 propionibac
16	40	58.0	361 16 09ZPFR9	09ZPFR9 listeria in

17	40	58.0	362 16 0981G4	0981G4 rhizobium l
18	40	58.0	453 16 09JZY9	09JZY9 neisseria m
19	40	58.0	433 16 09JY08	09JY08 neisseria m
20	40	58.0	506 10 09SKW7	09SKW7 zea mays (m
21	40	58.0	570 10 09PEA2	09PEA2 arabidopsis
22	40	58.0	570 10 0940P6	0940P6 arabidopsis
23	40	58.0	627 10 09MA10	09MA10 arabidopsis
24	40	58.0	976 2 054222	054222 staphylococ
25	40	58.0	1723 5 08WRD0	08WRD0 plasmodium
26	39	56.5	162 16 09P0K0	09P0K0 ureaplasma
27	39	56.5	230 16 09EW10	09EW10 streptomyces
28	39	56.5	277 16 09Z7B2	09Z7B2 chlamydia p
29	39	56.5	293 12 067573	067573 bean golden
30	39	56.5	338 3 074732	074732 schizosacch
31	39	56.5	439 12 09YW57	09YW57 melanoplus
32	39	56.5	446 16 09Z6P3	09Z6P3 listeria in
33	39	56.5	487 3 005377	005377 saccharomyc
34	39	56.5	492 3 012317	012317 saccharomyc
35	39	56.5	499 10 09SWE3	09SWE3 nicotiana t
36	39	56.5	528 3 005378	005378 saccharomyc
37	39	56.5	569 16 0980M0	0980M0 mycoplasma
38	39	56.5	660 2 045923	045923 clostridium
39	39	56.5	694 5 08T4D2	08T4D2 dirosophila
40	39	56.5	770 5 09VNT2	09VNT2 dirosophila
41	39	56.5	840 3 013652	013652 schizosacch
42	39	56.5	879 5 09G0J9	09G0J9 leishmania
43	39	56.5	1012 5 097035	097035 hydra magni
44	39	56.5	1048 3 012037	012037 saccharomyc
45	39	56.5	1169 5 09N1S0	09N1S0 toxoplasma

ALIGNMENTS

RESULT 1
ID 08R6X0 PRELIMINARY: PRT: 508 AA.
AC 08R6X0;
DT 01-JUN-2002 (TREMBLrel, 21, Created)
DT 01-JUN-2002 (TREMBLrel, 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel, 21, Last annotation update)
DE Hypothetical protein TTE2663.
GN TTE2663.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013206; AAM25782.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 508 AA: 58270 MW: BCBB3664EB79D845 CRC64;
Query Match 68.1%; Score 47; DB 16; Length 508;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKKKKKLLKS 13
Db 310 LYKKKKKKLLKVA 321
RESULT 2
ID 09Z655 PRELIMINARY: PRT: 215 AA.
AC 09Z655;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE Hypothetical 25.2 kDa protein.
 OC Zymomonas mobilis.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Zymomonas.
 OC NCBI_Taxid=542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ZM4;
 RA Um H.W., Kang H.S.;
 RT "Sequence analysis of 4349 fosmid clone of Zymomonas mobilis ZM4."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF102543; AAD19422.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 215 AA; 25210 MW; 48D308672D9A05B CRC64;

Query Match
 Best Local Similarity 72.7%; Score 44; DB 2; Length 215;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALYKKRNKLK 12
 Db 36 LFKSKAKLKK 46

RESULT 3
 ID 004578 PRELIMINARY; PRT; 827 AA.
 AC 004578;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE F19K23.6 protein.
 GN F19K23.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Osborne B.I., Vysotskaia V.S., Toriumi M., Yu G., Oji O., Shen Y.K.,
 RA Arango R., Au M., Buehler E., Conway A.B., Conway A.R., Dewar K.,
 RA Feng J., Kim C., Kurtz D., Li Y., Shin P., Sun H., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;
 RT "The sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1."
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC000375; AAB60760.1; -
 DR InterPro: IPR003690; mTERF.
 DR InterPro: IPR003880; Plantae_attach.
 DR Pfam: PF02536; mTERF. 2.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
 SQ SEQUENCE 827 AA; 92517 MW; 0D53CB85234555B CRC64;

Query Match
 Best Local Similarity 63.8%; Score 44; DB 10; Length 827;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKKRNKLK 13
 Db 282 AMFKKPNILTKS 294

RESULT 4
 080024

ID 080024 PRELIMINARY; PRT; 1891 AA.
 AC 080024;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Nonstructural polyprotein 123.
 OC Sindbis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 OC NCBI_Taxid=11034;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MRE16;
 RA Myles K.M., Pietro D.J., Olson K.E.;
 RT "Virus produced from a full-length, molecular clone of the Malaysian
 RT Sindbis virus, MRE16, efficiently infects Aedes aegypti and Culex
 RT tritaeniorhynchus by the oral route."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF492770; AAM10975.1; -
 KW Polyprotein.
 FT CHAIN 1 540 NSP1.
 FT CHAIN 541 1347 NSP2.
 FT CHAIN 1348 1891 NSP3.
 SQ SEQUENCE 1891 AA; 210105 MW; 07ED7460B87FBBC0 CRC64;

Query Match
 Best Local Similarity 62.3%; Score 43; DB 12; Length 1891;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 ALYKKRNKLK 13
 Db 1383 ALYKKPNSEFVS 1395

RESULT 5
 ID 080023 PRELIMINARY; PRT; 2508 AA.
 AC 080023;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Nonstructural polyprotein 1234 (Fragment).
 OS Sindbis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 OC NCBI_Taxid=11034;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MRE16;
 RA Myles K.M., Pietro D.J., Olson K.E.;
 RT "Virus produced from a full-length, molecular clone of the Malaysian
 RT Sindbis virus, MRE16, efficiently infects Aedes aegypti and Culex
 RT tritaeniorhynchus by the oral route."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF492770; AAM10974.1; -
 KW Polyprotein.
 FT CHAIN 1 >540 NSP1.
 FT CHAIN 541 >1347 NSP2.
 FT CHAIN 1348 >1898 NSP3.
 FT CHAIN 1899 >2506 NSP4.
 FT NON_TER 2508 2508
 SQ SEQUENCE 2508 AA; 279395 MW; D3F55794FABF740 CRC64;

Query Match
 Best Local Similarity 62.3%; Score 43; DB 12; Length 2508;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 ALYKKRNKLK 13
 Db 1383 ALYKKPNSEFVS 1395

RESULT 6

067584
ID Q67584 PRELIMINARY: PRT: 293 AA.
AC Q67584;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN BL1 protein.
GN BL1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration."
RT Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
RT hybridization probes and aspects of bean golden mosaic in Brazil."
RT Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
RT disease: The nucleotide sequence of the infectious cloned DNA
RT components of a Brazilian isolate of bean golden mosaic geminivirus."
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M88687; AAA46317.1; -;
DR InterPro: IPR000211; GeminL.B1.
DR Pfam: PF00845; GeminL.B1; 1.
SQ SEQUENCE 293 AA: 33049 MW: FER2D53583984854 CRC64;

Query Match 60.9%; Score 42; DB 12; Length 293;
Best Local Similarity 63.6%; Pred. No. 54;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKWKXKLK 13
Db 178 YKKWKXKLK 188

RESULT 7
ID Q9L196 PRELIMINARY: PRT: 107 AA.
AC Q9L196;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Genomic DNA, chromosome 3, pl clone:IMB010.
OS Arabidopsis thaliana (mouse-ear cress).
OU Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA MEDLINE=20363099; PubMed=10907853;
RX Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones.";

RL DNA Res. 7:217-221(2000).
DR EMBL; AP001309; BAB02593.1; -;
SQ SEQUENCE 107 AA: 12145 MW: 020DD58429B14BC CRC64;

Query Match 59.4%; Score 41; DB 10; Length 107;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKWKXKLK 11
Db 96 HKKWKXKV 104

RESULT 8
ID Q98PE3 PRELIMINARY: PRT: 286 AA.
AC Q98PE3;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
GN MYPU_7800.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chembud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis."
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445565; CAC13953.1; -;
DR Mypulist; MYPU_7800; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 286 AA: 34833 MW: 17BAE37548A9C081 CRC64;

Query Match 59.4%; Score 41; DB 16; Length 286;
Best Local Similarity 54.5%; Pred. No. 76;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKXKLK 12
Db 137 IHKWKXKLK 147

RESULT 9
ID Q9KH70 PRELIMINARY: PRT: 307 AA.
AC Q9KH70;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Thermostable dipeptidase Bdp.
GN BDP.
OS Brevibacillus borstelensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Penibacillaceae; Brevibacillus.
OX NCBI_TaxID=45462;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BGS-1;
RA Kwon S., Hong S., Sung M.;
RT "A Novel Thermostable Dipeptidase from Brevibacillus borstelensis BGS-
RT 1.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP268476; AAF97793.1; -;
DR InterPro: IPR000180; Renal_dipeptidase.
DR Pfam: PF01244; Renal_dipeptidase; 1.

SQ SEQUENCE 307 AA: 34975 MW: 502PCC83754E20E2 CRC64;
 Query Match 59.4%; Score 41; DB 2; Length 307;
 Best Local Similarity 77.8%; Pred. No. 81;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKMK 9
 |||||
 Db 10 ALYKKMK 18

RESULT 10
 ID 08V3P3 PRELIMINARY; PRT; 439 AA.
 AC 08V3P3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE SPV051 hypothetical protein.
 GN SPV051.
 OS Swinepox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Suipoxvirus.
 NCBI_TaxID=10276;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17077-99;
 RX MEDLINE=21624277; PubMed=1152168;
 RA Atonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Ballinsky C.,
 RA Kutish G.F., Rock D.L.;
 RT "The genome of swinepox virus."
 RL J. Virol. 76:783-790(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17077-99;
 RA Atonso C.L., Tulman E.R., Lu Z., Ballinsky C., Osorio F.A., Zsak L.,
 RA Kutish G.F., Rock D.L.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF410153; AAL69790.1;
 KW Hypothetical protein.
 SQ SEQUENCE 439 AA: 50984 MW: 4991293795BF3850 CRC64;

Query Match 59.4%; Score 41; DB 12; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1; Le+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALYKKMK 7
 |||||
 Db 325 ALYKKMK 331

RESULT 11
 ID 074858 PRELIMINARY; PRT; 531 AA.
 AC 074858;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Lysyl-tRNA synthetase.
 GN SPC18.08.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Hilbert H., Duesterhoeft A., Wood V., Rajandream M.A., Barrell B.G.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA (AMINO ACID) = AMP +
 CC DIPHOSPHATE + L-AMINOACYL-TRNA (AMINO ACID).
 CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

DR EMBL: AL031907; CAA21422.1;
 DR HSSP; P14825; IEP0.
 DR InterPro: IPR002106; AATRNA_LigaseII.
 DR InterPro: IPR004364; tRNA-synt_2.
 DR InterPro: IPR002313; tRNA-synt_lys-2.
 DR InterPro: IPR004365; tRNA-anti.
 DR Pfam: PF00152; tRNA-synt_2; 1.
 DR Pfam: PF01336; tRNA-anti; 1.
 DR PRINTS: PR00982; TRNASYNTHLYS.
 DR TIGRFAMs: TIGR00499; lysS_bact; 1.
 DR PROSITE: PS00179; AA-TRNA_LIGASE_II_1; 1.
 DR PROSITE: PS00339; AA-TRNA_LIGASE_II_2; UNKNOWN_1.
 KW Atp-binding; Aminoacyl-tRNA synthetase; Ligase; Protein biosynthesis.
 SQ SEQUENCE 531 AA: 60285 MW: AA8418CDF32C416F CRC64;

Query Match 59.4%; Score 41; DB 3; Length 531;
 Best Local Similarity 50.0%; Pred. No. 1; Le+02;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 LYKKMKKLKS 13
 :|||:|:|
 Db 66 ILEKMKKTKS 77

RESULT 12
 ID 09G8T2 PRELIMINARY; PRT; 762 AA.
 AC 09G8T2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Orf762.
 GN ORF762.
 OS Rhodomonas salina.
 OG Mitochondrion.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
 NCBI_TaxID=52970;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
 RT "Algae with secondary chloroplasts have mitochondria that originate
 RT from the host."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF288090; AAG17765.1;
 DR InterPro: IPR004442; Intron_maturase2.
 DR InterPro: IPR004477; RMTse.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF00078; rvt; 1.
 KW Mitochondrion; RNA-directed DNA polymerase.
 SQ SEQUENCE 762 AA: 87494 MW: 9235F3F7EDB04911 CRC64;

Query Match 59.4%; Score 41; DB 8; Length 762;
 Best Local Similarity 70.0%; Pred. No. 2; Le+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 KKKMKKLKS 13
 |:|:|:|
 Db 674 KKKMKKLKS 683

RESULT 13
 ID 092FK1 PRELIMINARY; PRT; 87 AA.
 AC 092FK1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein lin0103.
 GN LIN0103.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 NCBI_TaxID=1642;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CLIP 11262 / SEROVAR 6A;
 RX PubMed-11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Chablt A., Chetoui F., Couve E., de Darvar A., Dehoux H.,
 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Entian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,
 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
 Madueno E., Maounam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 Rammel B., Rose M., Schluter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria species*.";
 RL Science 294:849-852(2001).
 DR EMBL: AL596163: CAC95336.1: -
 DR Listlist: LIN00103: -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 87 AA; 10135 MW; E1A37A29CACE4DF CRC64;

Query Match 58.0%; Score 40; DB 16; Length 87;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 YKKWK 9
 DB 77 YKKWK 83

RESULT 14
 ID 08YGA3 PRELIMINARY; PRT; 170 AA.
 AC 08YGA3;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE DNB protein.
 GN BME11257.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed-11756688;
 RA Delvecchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
 Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyriakides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL: AE009564: AAL52438.1: -
 KW Complete proteome.
 SQ SEQUENCE 170 AA; 19976 MW; 448E7185D7860B66 CRC64;

Query Match 58.0%; Score 40; DB 16; Length 170;
 Best Local Similarity 63.6%; Pred. No. 66;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKKWK 11
 DB 9 AYYNOMANKL 19

RESULT 15
 ID P72185 PRELIMINARY; PRT; 259 AA.
 AC P72185;

DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 DE Repressor protein (HEMR protein).
 OS Hemr.
 OS Propionibacterium freudenreichii.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Propionibacteriaceae; Propionibacteriaceae;
 OC Propionibacterium.
 OX NCBI_TaxID=1744;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Roessner C.A.;
 RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 17-259 FROM N.A.
 RC STRAIN-IF012424;
 RX MEDLINE=93175878; PubMed=8439165;
 RA Murakami K., Hashimoto Y., Murooka Y.;
 RT "Cloning and characterization of the gene encoding glutamate 1-
 RT semialdehyde 2,1-aminomutase, which is involved in delta-
 RT aminolevulinic acid synthesis in *Propionibacterium freudenreichii*.";
 RL Appl. Environ. Microbiol. 59:347-350(1993).
 RN [3]
 RP SEQUENCE OF 17-259 FROM N.A.
 RC STRAIN-IF012424;
 RA Hashimoto Y., Yamashita Y., Ono H., Murooka Y.;
 RL J. Ferment. Bioeng. 82:93-100(1996).
 RN [4]
 RP SEQUENCE OF 17-259 FROM N.A.
 RC STRAIN-IF012424;
 RX MEDLINE=97306686; PubMed=9163953;
 RA Hashimoto Y., Yamashita Y., Murooka Y.;
 RT "The *Propionibacterium freudenreichii* hemYBXR gene cluster, which
 RT encodes enzymes and a regulator involved in the biosynthetic pathway
 RT from glutamate to protoheme.";
 RL Appl. Microbiol. Biotechnol. 47:385-392(1997).
 CC -i- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: U51164; AAB07865.1: -
 DR EMBL: D85417; BAA21913.1: -
 DR InterPro: IPR001647; HTH_Tetr.
 DR Pfam: PF00440; Tetr. 1.
 KW DNA-binding; Transcription regulation.
 SQ SEQUENCE 259 AA; 27426 MW; 5FCB0FF342606170 CRC64;

Query Match 58.0%; Score 40; DB 2; Length 259;
 Best Local Similarity 66.7%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKWK 9
 DB 76 ALYKRPWK 84

Search completed: December 30, 2002, 16:23:05
 Job time : 31 secs

